

Project Overview

Global analysis of functional units in plant chromosomes: DNA replication, domain structure, and transcription.

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The goals of this project are to characterize the core replication machinery of higher plants and to construct chromosomal maps of replication timing, origins, matrix attachment regions, modified histones, DNA methylation, and transcriptional activity. We are characterizing chromosomal domains in large portions of rice chromosomes 4 and 10 of rice and all of Arabidopsis chromosome 4. The grant has supported 27 research publications to date, plus one currently under review.

Scientific objectives and approaches – Plants have many advantages for studying eukaryotic DNA replication origins and their relationship to structural and transcriptional domains. Plants like Arabidopsis and rice have small genomes that have been or will be fully sequenced. Plant tissues at different stages of development and rapidly proliferating, synchronizable cultured cells are readily accessible in quantities amenable for bio-chemical analysis. We propose to exploit these properties to construct and overlay chromosomal maps of replication origins, matrix attachment regions, modified histones, DNA methylation levels and transcription. These experiments will combine powerful microarray technologies with molecular, cellular and immunological tools to generate functional maps for the short arm of rice chromosome 1 and all of Arabidopsis chromosome 4. We will generate and compare maps from cultured cells at different stages of the division cycle. Comparison of these maps with each other and with data for other eukaryotes will provide insight into chromosomal features conserved among all eukaryotes and identify characteristics unique to the plant kingdom. We will also generate maps from rice intercalary meristem and developing endosperm. These maps will provide insight into

developmental changes in origin use and their relation to transcription and chromatin structure changes.

Broader impact – This project brings together investigators with a unique combination of interests and expertise to explore the functional genomics of plant chromosomes. Our results will define chromosomal domains for DNA replication, chromatin structure and transcription, and serve as basis for future studies on more complex plant and animal genomes. It will also provide a foundation for developing new transformation and gene targeting methods, plant artificial chromosome vectors, and related technologies that will help support a new generation of genetic engineering technologies. The project will generate new genomic information and tools that will be accessible to other members of the plant science community via the web. The genomic arrays for rice and Arabidopsis designed as part of this project will be available to the community. The project will provide training at the undergraduate, graduate and postdoctoral levels in state-of-the-art functional genomic and bioinformatics techniques. We will conduct workshops on genomic analysis tools that will be accessible to scientists in the south-eastern US and to faculty and students at historically black and minority institutions. With funding from an outreach supplement, we are also working with North Carolina educators to develop teaching tools and an instructional manual for presenting genomics concepts to middle school students.